

47

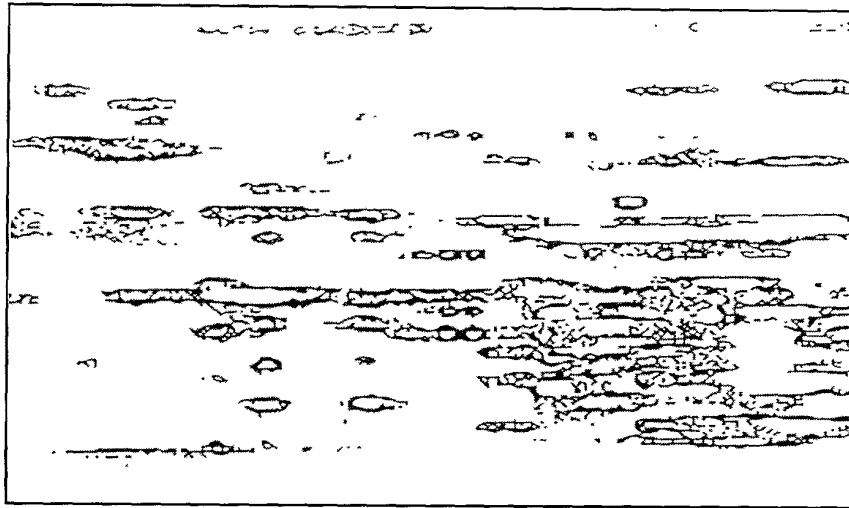


FIG. 1A

09983020 09/983020

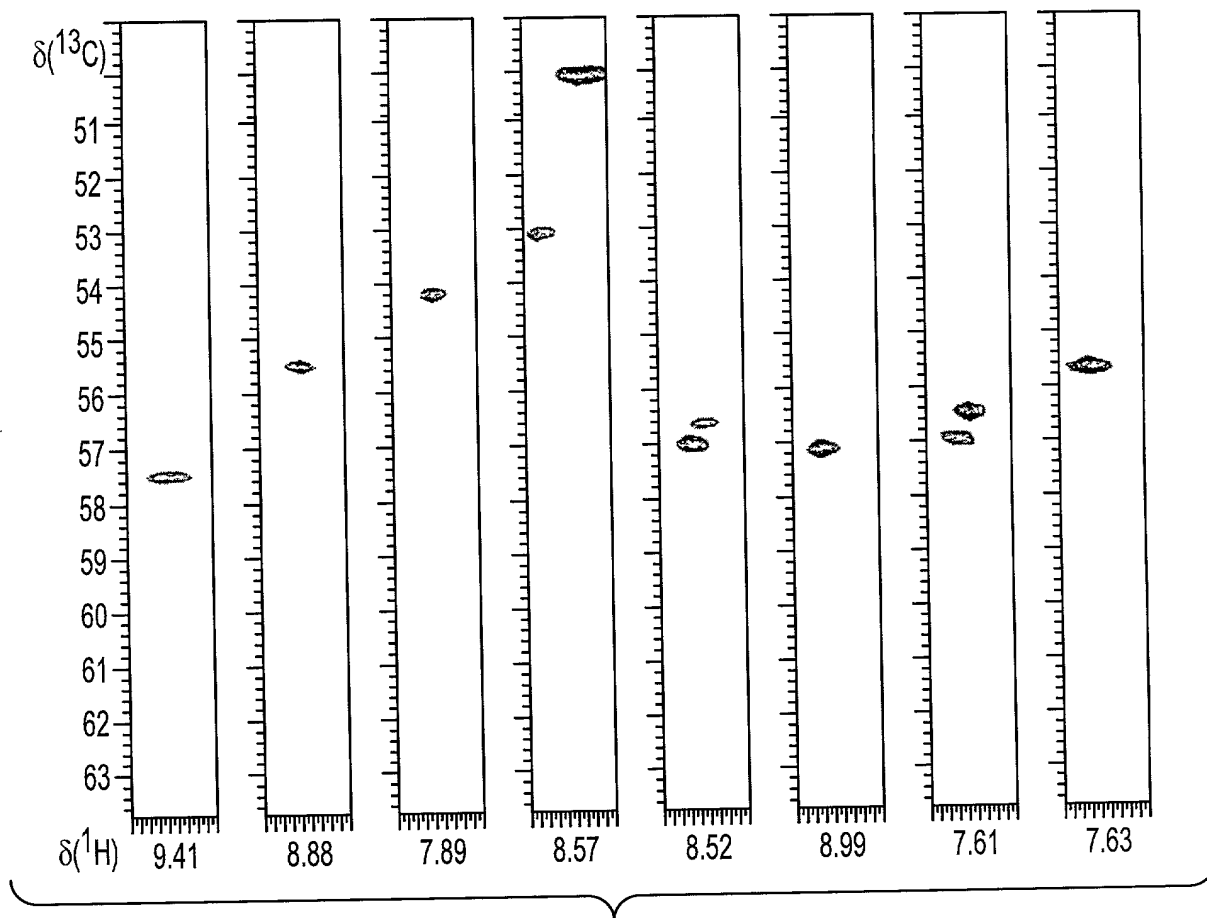


FIG. 1B

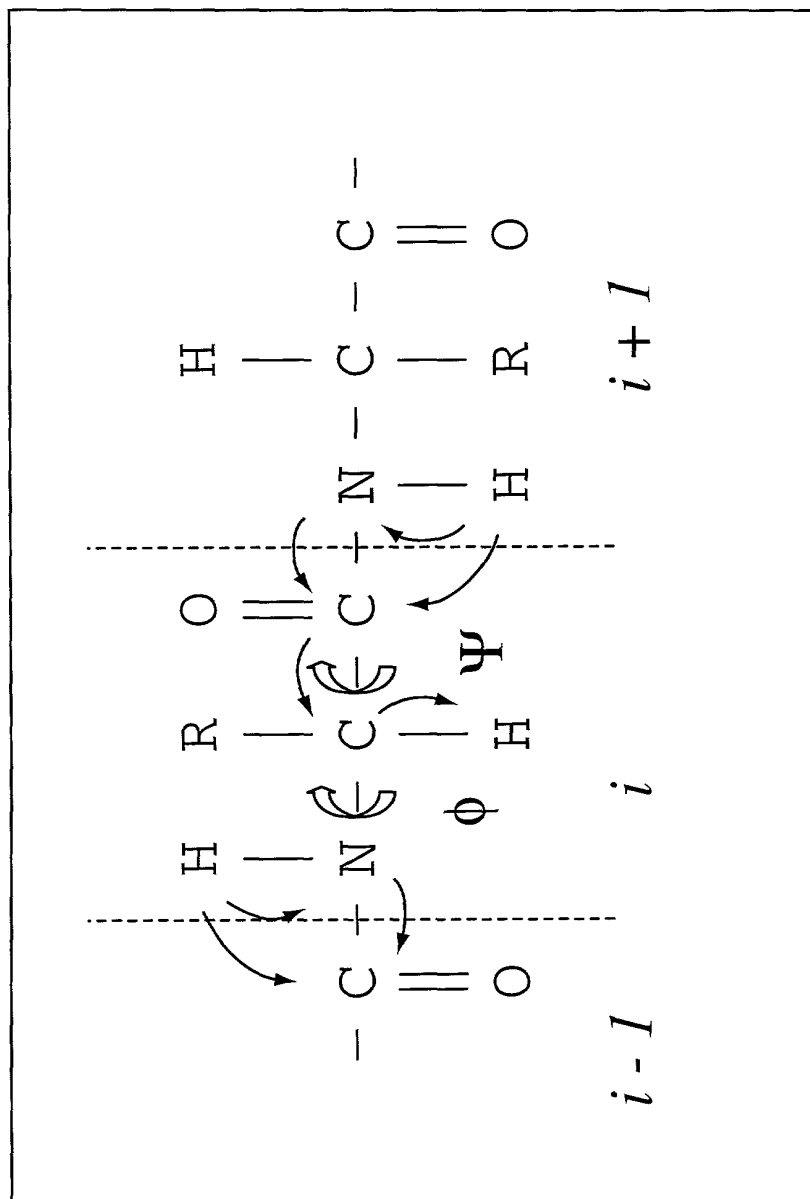


FIG. 2

205120 00000000

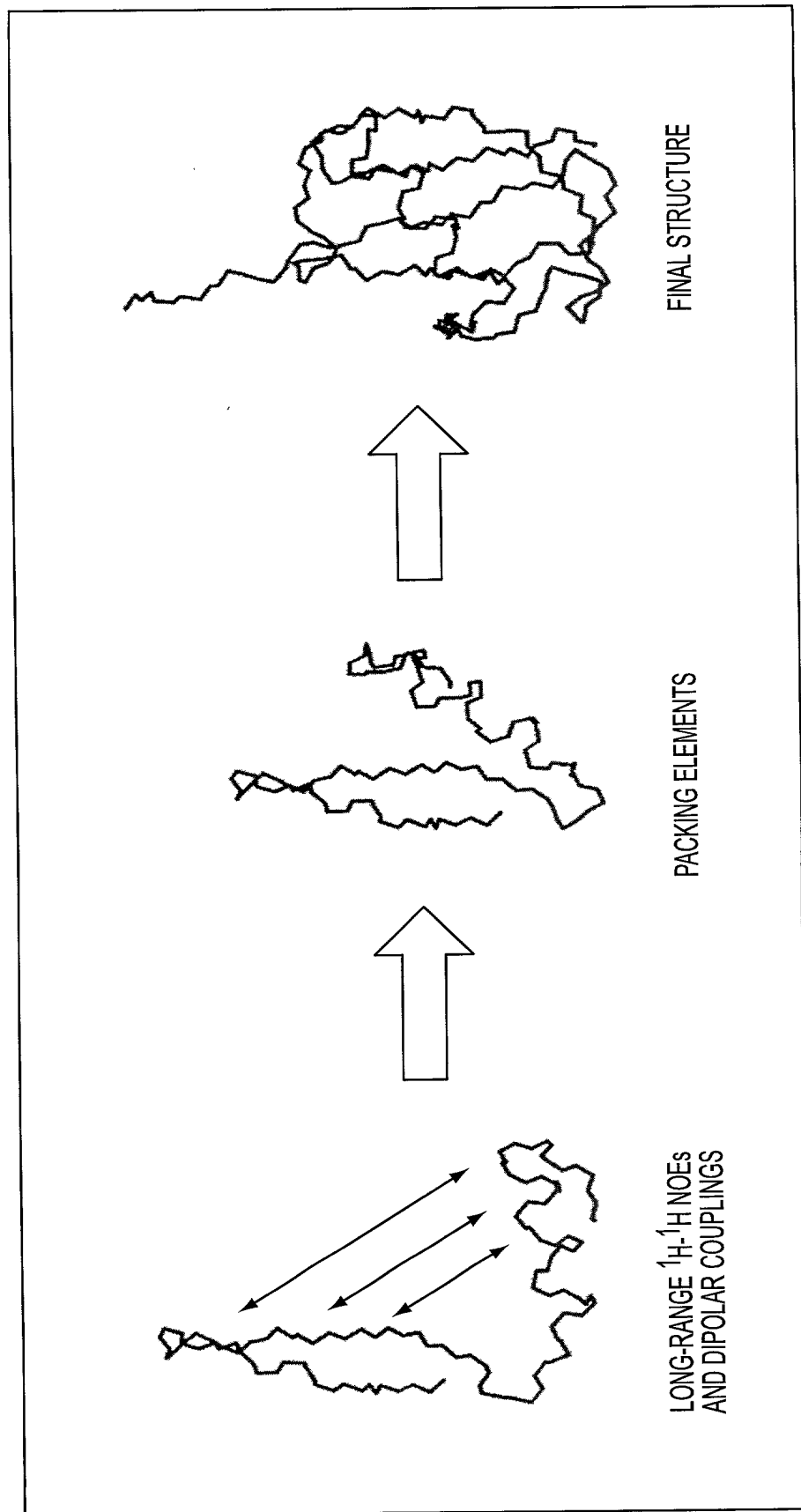
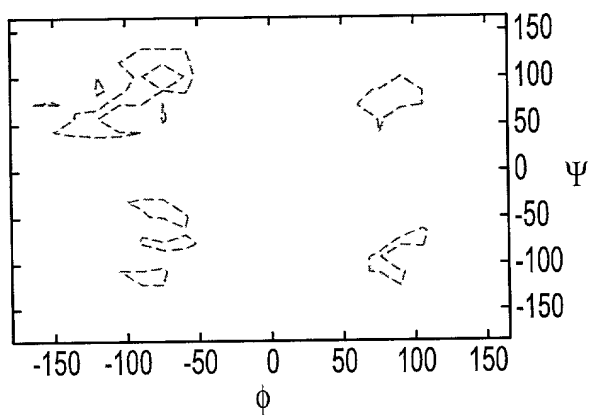
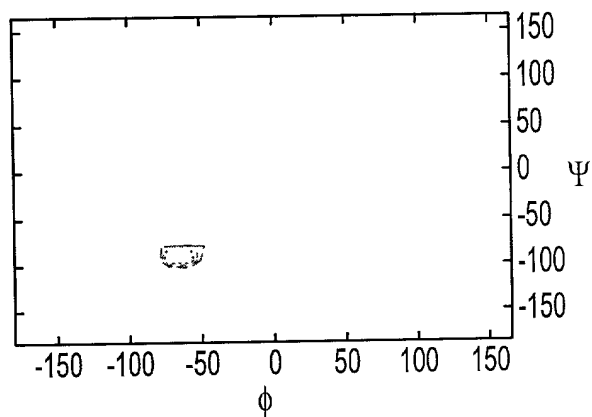
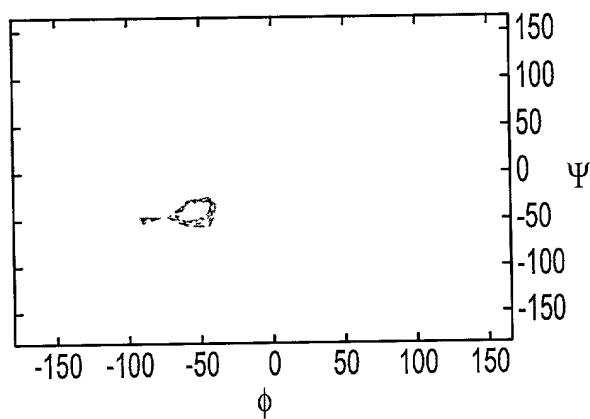
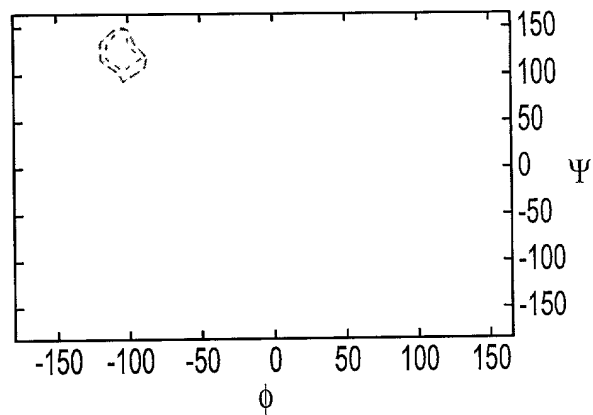
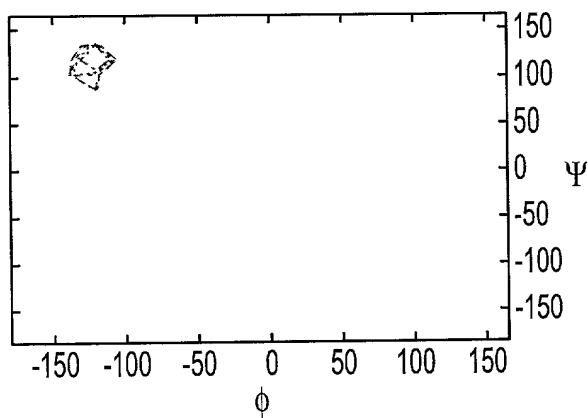


FIG. 3



205120 0203650

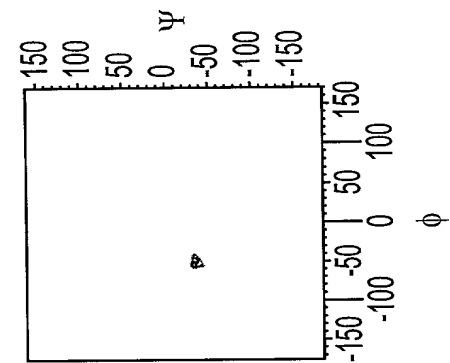


FIG. 5A

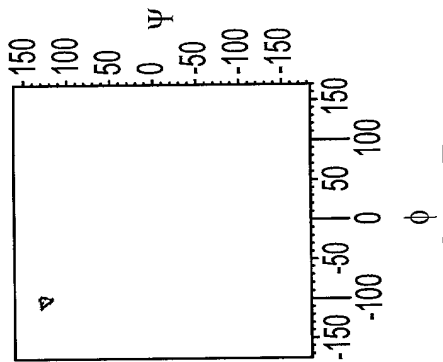


FIG. 5B

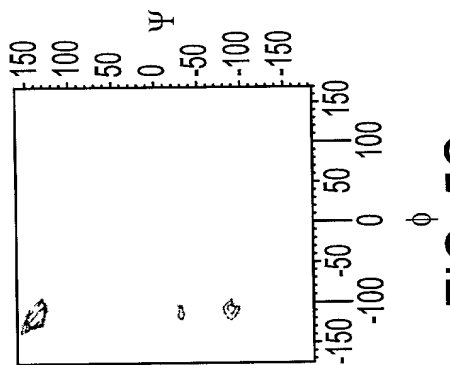


FIG. 5C

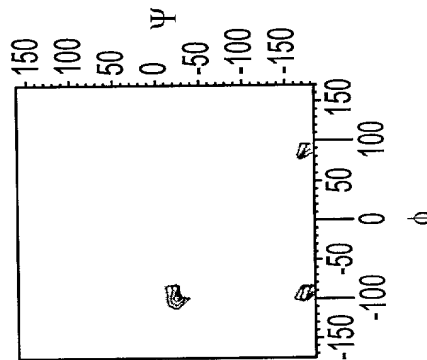


FIG. 5E

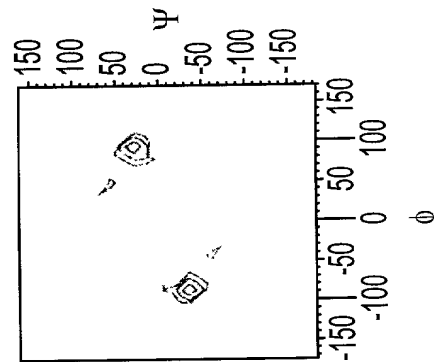


FIG. 5F

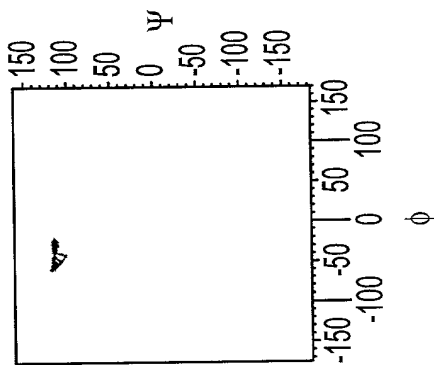


FIG. 5G

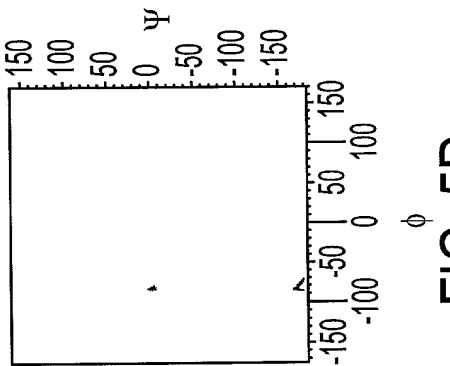


FIG. 5D

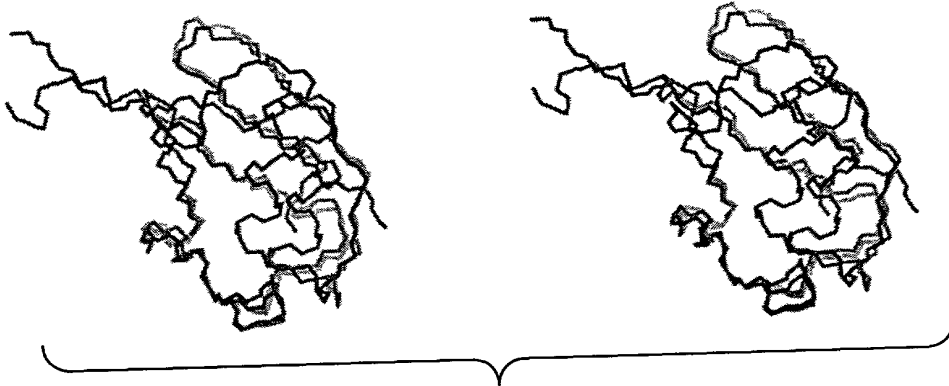


FIG. 6A

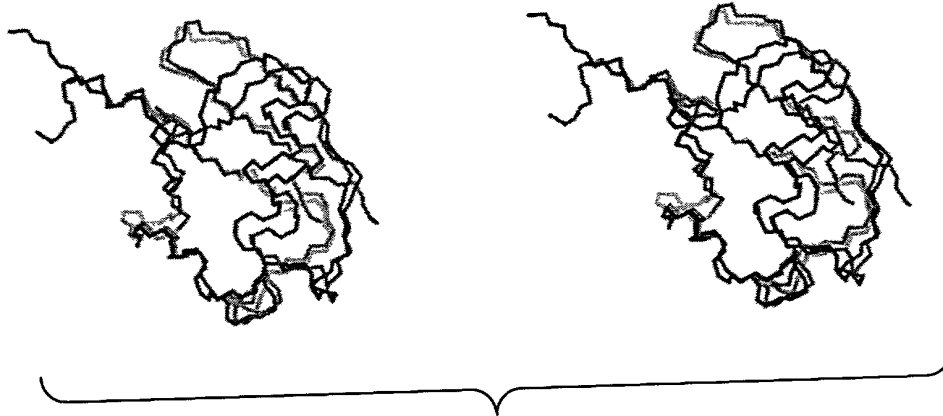


FIG. 6B

09983020.021502

GENERATE LINEAR
AMINO-ACID CHAIN

CALCULATE ϕ , ψ ANGLES FOR
EACH PEPTIDE PAIR USING
EXPERIMENTAL RESIDUAL
DIPOLAR COUPLINGS

FOLD LINEAR SEQUENCE WITH
DIHEDRAL ANGLE AND
BACKBONE NOE RESTRAINTS

REFINE STRUCTURE USING
NOE AND DIPOLAR COUPLING
RESTRAINTS

FIG. 7

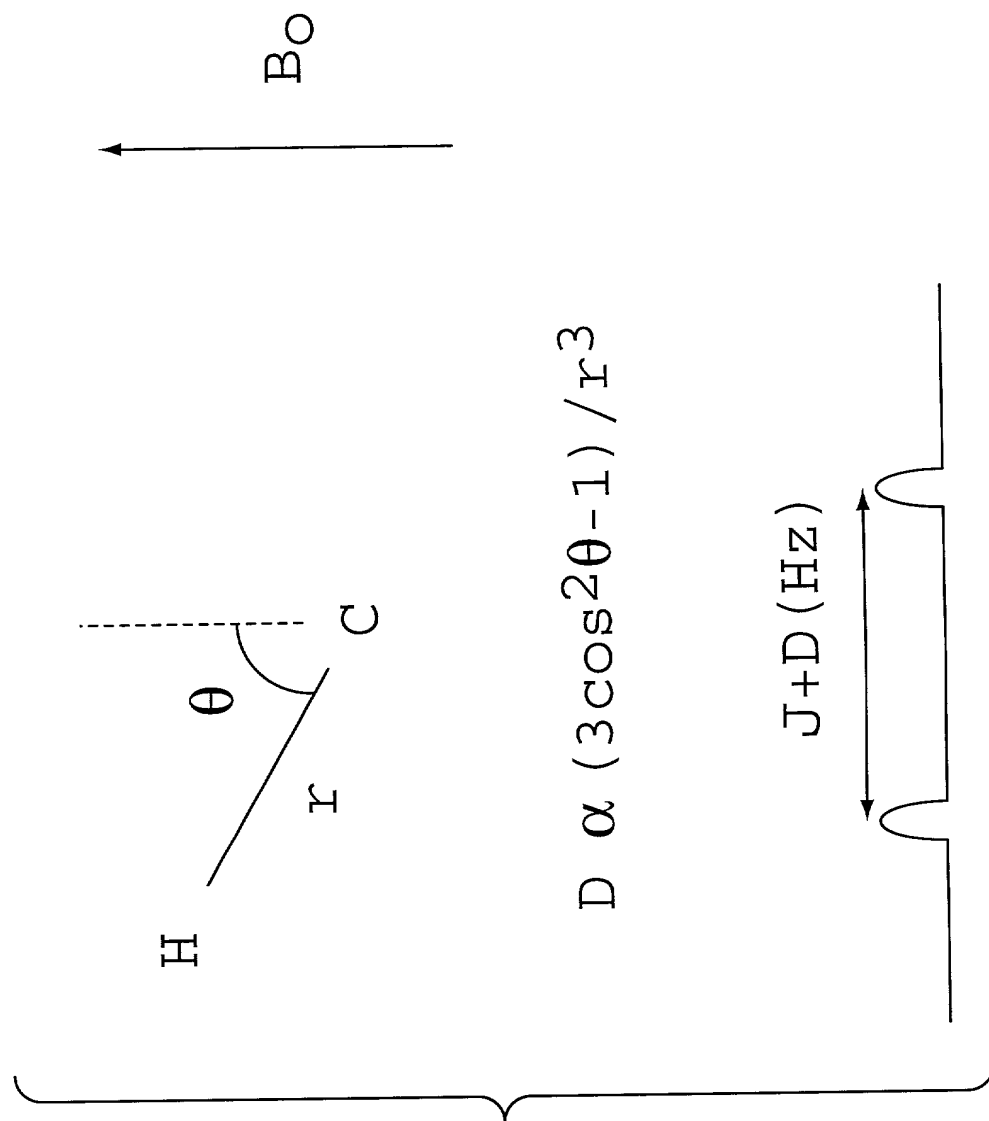


FIG. 8

0205120" 020E8660

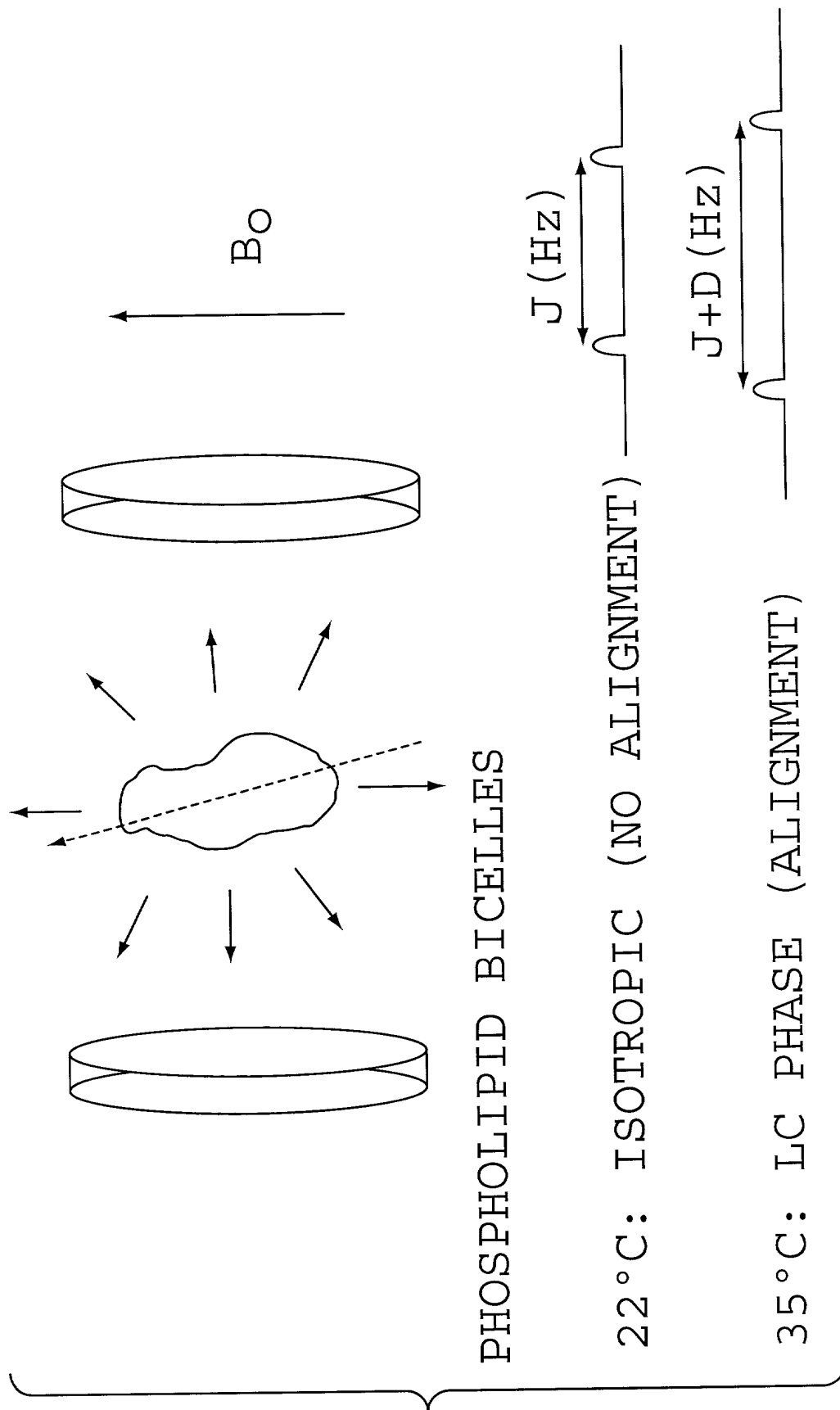
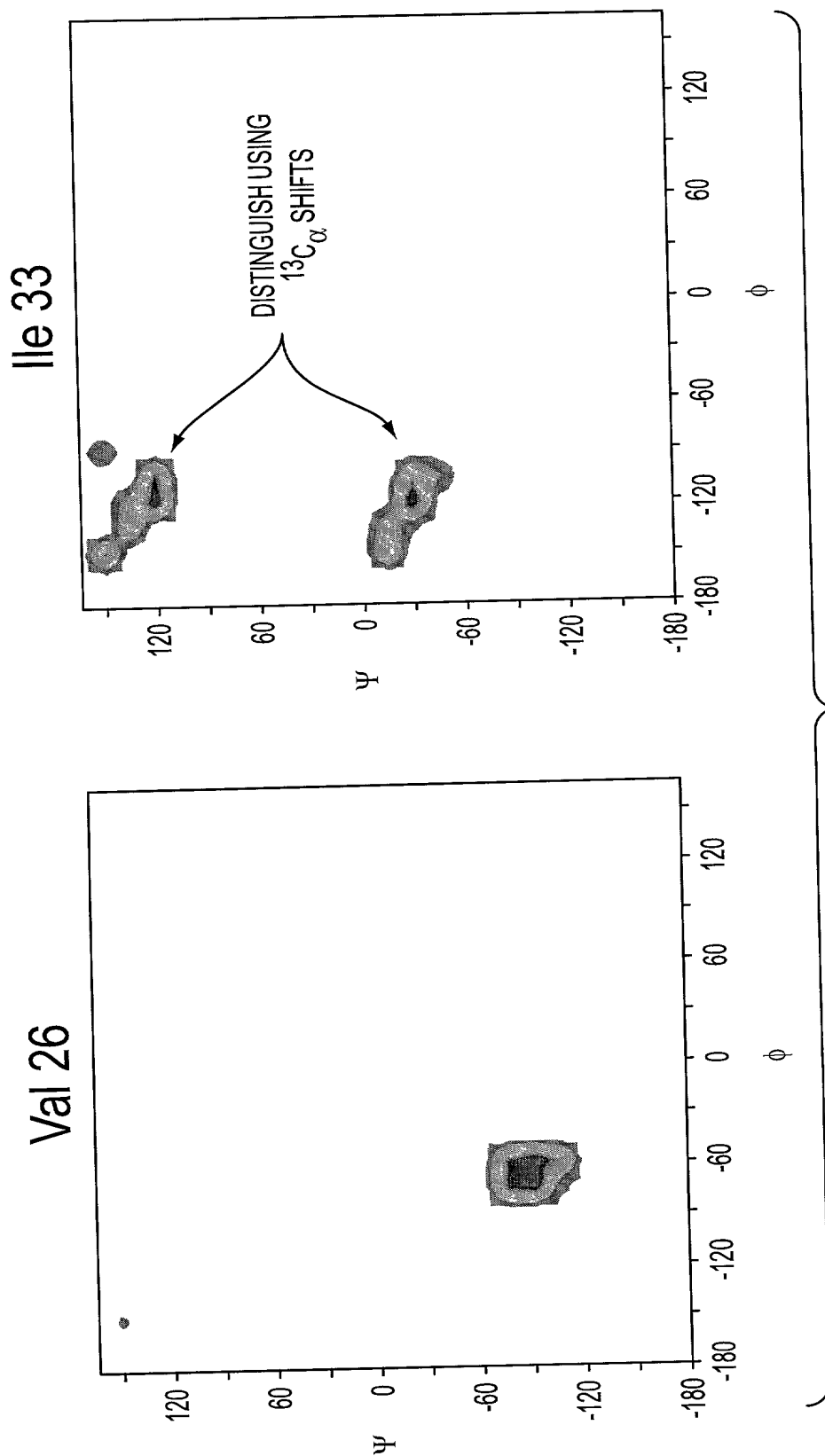


FIG. 9



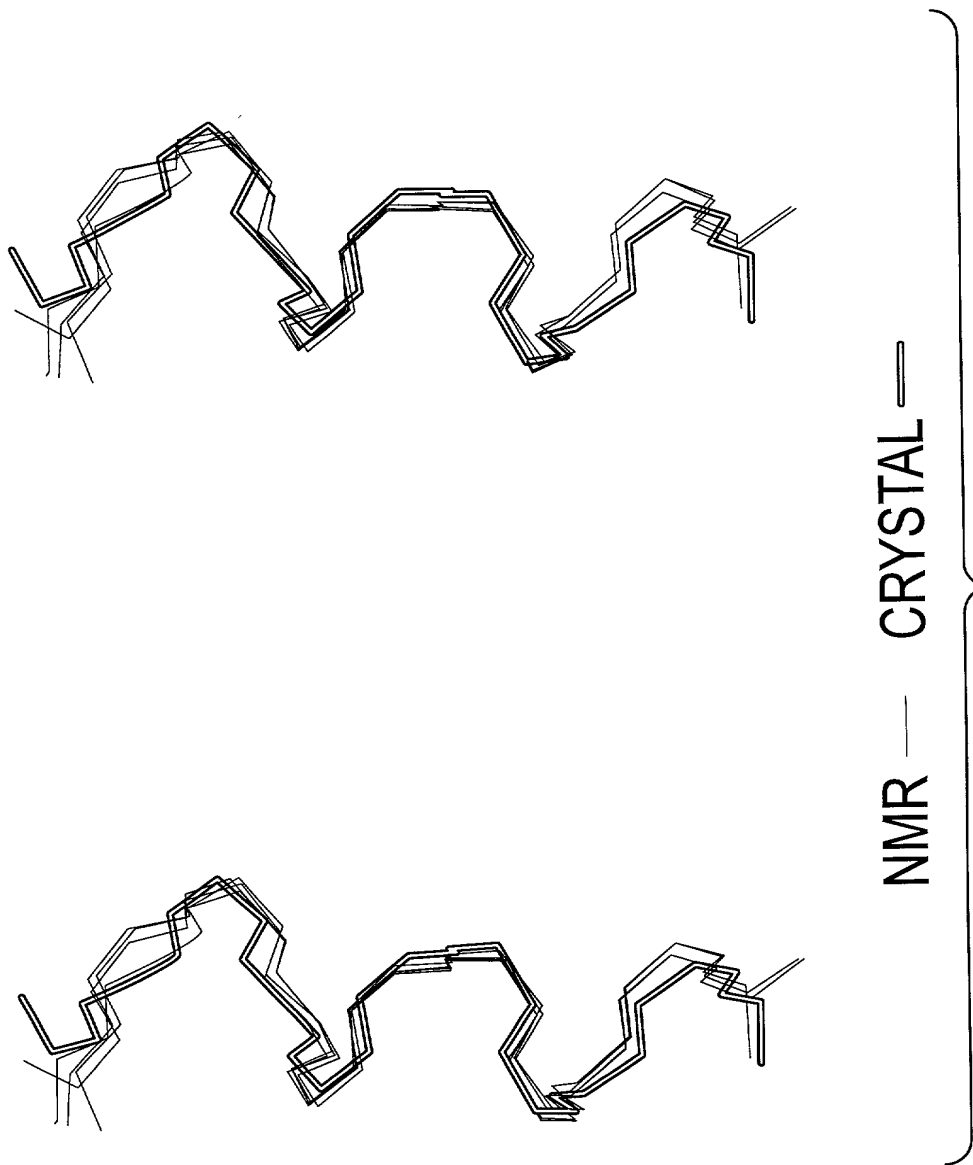


FIG. 11

005120" 020E8660

0205T20" 020E8660

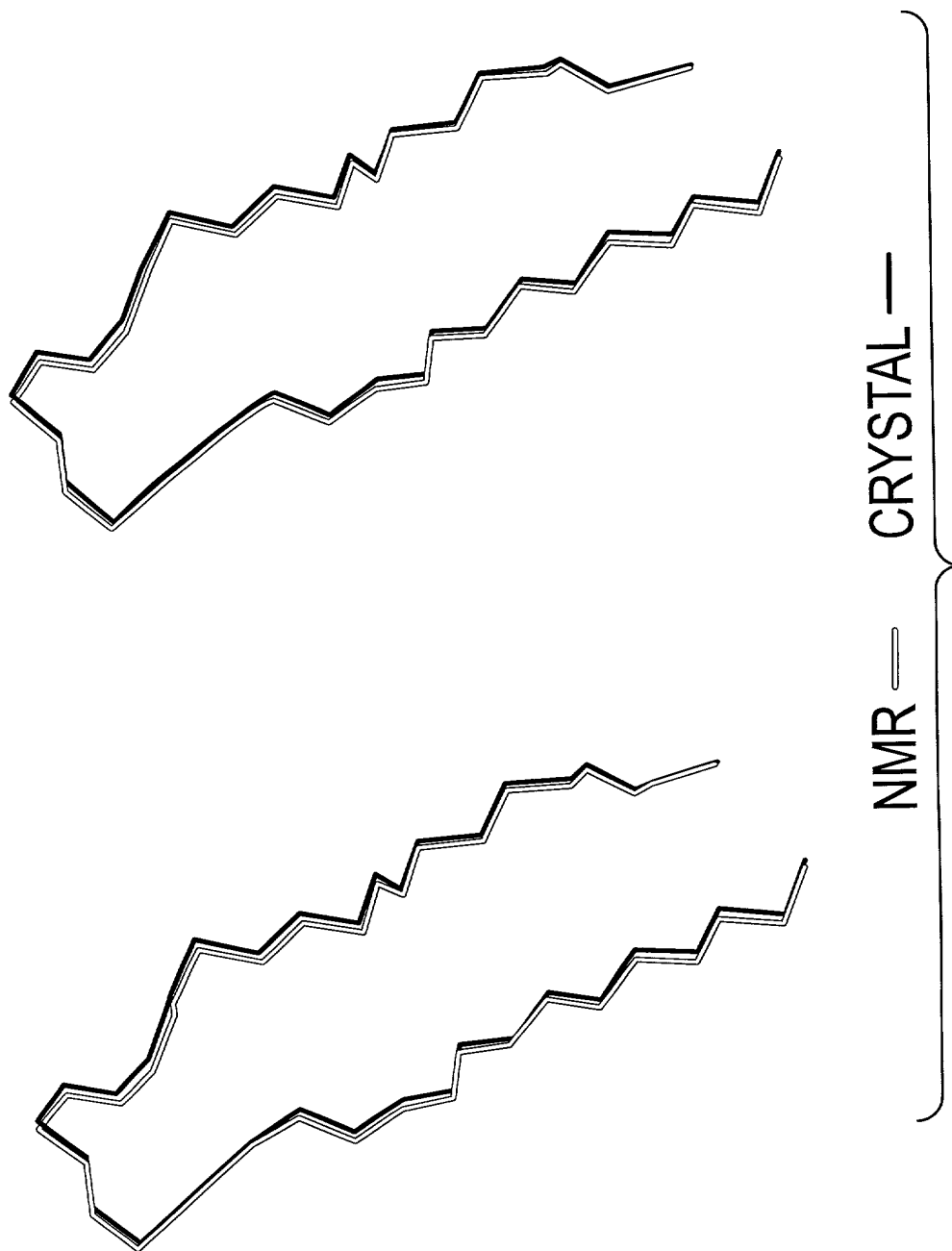


FIG. 12

205120" 020E3660

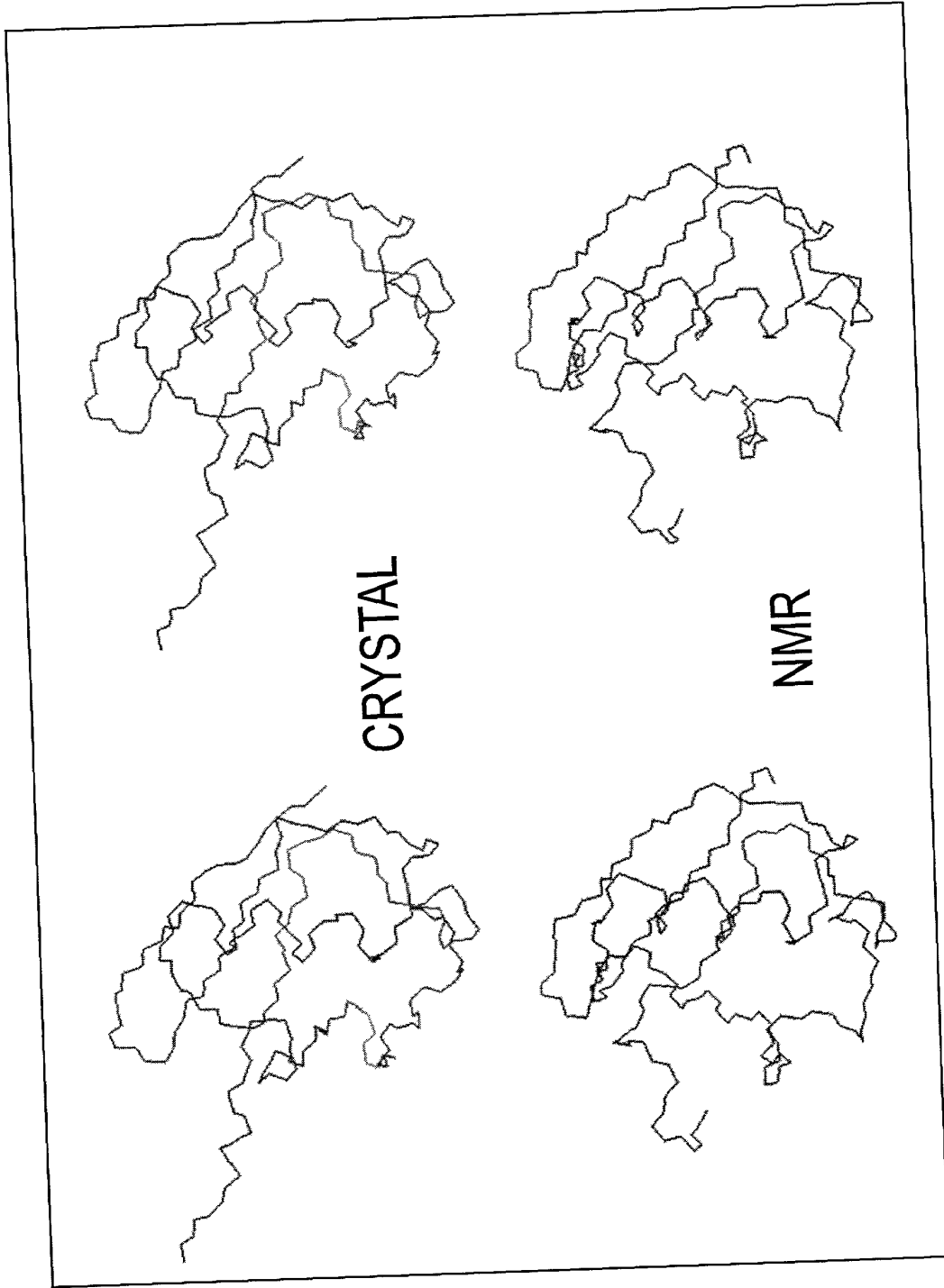


FIG. 13